

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_P2n model

Run on: October 8, 2003, 16:28:28 ; Search time 343.211 Seconds
(without alignments)
3964.081 Million cell updates/sec

Title: US-10-001-848-3

Perfect score: 2709

Sequence: 1 MTPSPULLLNPPLLGAPP.....HSHTHSHVEGKVKHQHIIHYQC 504

Scoring table: BLASTM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs., 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing First 45 summaries:

Command line parameters:
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Database : N_GenSeq_19Jun03::

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and is derived by analysis of the total score distribution.

SUMMARIES

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	2	2709	100.0	3169	22	AAF27781
	3	2709	100.0	3402	21	AAC58376
	4	2709	100.0	3402	21	AAZ64984
	5	2709	100.0	3402	22	AAF44130
	6	2709	100.0	3402	24	ABK11750
	7	2709	100.0	3402	24	ABK28591
	8	2709	100.0	3402	25	ABX80198
	9	2709	100.0	3402	25	ABX81085
	10	2709	100.0	3402	25	ABX90175
	11	2709	100.0	3402	25	ABX77286
	12	2709	100.0	3402	25	ABX79382
	13	2709	100.0	3402	25	ABX6421
	14	2709	100.0	3402	25	ABX16285
	15	2709	100.0	3101	24	ABQ78867
	16	2701	99.7	3112	24	AAK28842
	17	2694	99.4	3138	25	ABX34717
	18	2694	99.4	2456	23	AAS14936
	19	2694	92.9	91.1	22	AAI57799
	20	2468.5	91.1	3186	22	AAI96724
	21	2357	87.0	1967	21	AAI96724
	22	2357	87.0	2274	22	ABQ78868
	23	2357	87.0	2277	23	AAS14935
	24	2095	77.3	2178	22	AAH76316
	25	2417.7	71.9	2417.7	24	ABQ78869
	26	1877	69.3	1177	22	AAH99452
	27	1877	69.3	1177	22	AAI59585
	28	1822	67.3	1742	21	AAA96725
	29	1821	67.2	1788	23	AAS14339
	30	1755	64.8	2556	24	ABO54233
	31	1755	64.8	2559	21	AAF16334
	32	1650	60.9	1004	21	AAA96726
	33	1496.5	55.2	1423	21	AAA96739
	34	882	32.6	624	22	AAF27784
	35	882	32.6	1074	22	ABP27783
	36	861	31.8	493	24	ABV9447
	37	831	30.7	854	22	AAD34802

ALIGNMENTS

RESULT 1

Human MANGO 003 coding sequence SBQ ID NO: 6 .
ID AAF27782 standard; cDNA; 1512 BP.
AC AAF27782;
XX 05-APR-2001 (first entry)

Membrane associated protein; secreted protein; human; mouse; rat;
INTRECEPT 340; MANGO 347; TANGO 272; TANGO 295; TANGO 354;
skel disorder; cardiovascular disorder; renal disorder; hepatic disorder;
haematopoietic disease; ss.
neoplastic disease; ss.
OS Homo sapiens.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

RESULT 2

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 8, 2003, 16:29:18 ; Search time 3342.44 Seconds
(without alignment)
4381.722 Million cell updates/sec

Title: US-10-001-848-3_COPY_18_375
Perfect score: 1894
Sequence: 1 AFPPAAARGPPKADKVVP.....LPDPKPPGPVASSSSATSL 358

Scoring table: BLOSUM62
Xgapop 10.0 ; Ygapop 10.0 ; Fgapop 6.0 ; Delop 6.0 ; Deletxt 7.0

Searched: 288711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-UNITS=bits -START=1 END=-1 -MATRIX=bIobum62 TRANS=human40_cdi -LIST=45
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11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: em_vii:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_p1:*

26: em_ro:*

27: em_sts:*

28: em_un:*

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29: em_vii:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_lrn:*
35: em_htg_fod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_htg:*
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40: em_htgo_mus:*
41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1894	100 0	1450	6	AX28796	AX28796 Sequence	
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3	1894	100 0	3402	6	AR252460	AR252460 Sequence	
4	1894	100 0	3402	6	AX080803	AX080803 Sequence	
5	1894	100 0	3402	6	AX191426	AX191426 Sequence	
6	1894	100 0	3402	6	AX403231	AX403231 Sequence	
7	1886	99 6	1565	9	AF279689	AF279689 Homo sapi	
8	1886	99 6	3080	6	AX287610	AX287610 Sequence	
9	1886	99 6	3080	9	HSA277437	HSA277437 Homo sapi	
10	1886	99 6	3112	6	AX287608	AX287608 Sequence	
11	1886	99 6	3397	9	AF312678	AF312678 Homo sapi	
12	1785	94 2	1967	6	AR156834	AR156834 Sequence	
13	1785	94 2	2274	10	MMU293947	MMU293947 Mus muscu	
14	1785	94 2	2277	6	AX287593	AX287593 Sequence	
15	1785	94 2	2359	10	AF213100	AF213100 Mus muscu	
16	1767	93 3	1788	6	AX287613	AX287613 Sequence	
17	1566	82 7	1004	6	AR156836	AR156836 Sequence	
18	1414 5	74 7	177950	9	AC019103	AC019103 Homo sapi	
19	1414 5	74 7	32256	10	AF321302	AF321302 Mus muscu	
20	1410 5	74 5	24181	10	MMU108490	MMU108490 Mus muscu	
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c	22	1410 5	74 5	176874	AC123743	AC123743 Mus muscu	
c	23	1402 5	74 0	2774	5	BC053245	BC053245 Danio rer
c	24	1402 5	74 0	187234	2	AC117047	AC117047 Rattus no
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c	26	1364 4	72 0	2178	6	AX224732	AX224732 Sequence
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c	28	1290 1	68 1	2339	10	AF321301	AF321301 Mus muscu
c	29	1279 5	67 6	1742	6	AR156835	AR156835 Sequence
c	30	1164 5	61 5	781	6	AX080801	AX080801 Sequence
c	31	1154 5	61 0	182635	2	AC140291	AC140291 Mus muscu
c	32	861 1	45 5	3493	6	AX318742	AX318742 Sequence
c	33	61 1	32 3	384	6	AR156833	AR156833 Sequence
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c	36	52 4	27 7	204579	2	AL954843	AL954843 Danio rer
c	37	49 2	26 0	3002	5	AF157560	AF157560 Danio rer
c	38	48 7	25 7	3468	5	PWFGPR4	PWFGPR4
c	39	48 4	25 6	2763	5	PWFGPR3	PWFGPR3
c	40	48 2	25 5	3634	5	XLU24491	XLU24491
c	41	48 2	25 5	3815	5	XELXIFGFR	XELXIFGFR
c	42	47 5	25 1	2520	10	S56291	S56291 Sam3-PGF3
c	43	47 5	25 1	4156	10	BC053056	BC053056 Mus muscu
c	44	47 5	25 1	4158	6	MUSMFR3	MUSMFR3
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ALIGNMENTS

RESULT 1

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 DEFINITION Sequence 4 from Patent WO1707977.
 ACCESSION AX287596
 VERSION AX287596.1 GI:17049361
 KEYWORDS Homo sapiens (human)
 ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Saris C.M., Mu, S.X., Xia, M., Boone, T.C. and Covey, T.
 Fibroblast growth factor receptor-like molecules and uses thereof
 Patent: WO 017077-A-4 27-SEP-2001
 Amgen, Inc. (US) ; Saris, Christian M. (US) ; Mu, Sharon X. (US) ;
 Xia, Min (US) ; Boone, Thomas Charles (US) ; Covey, Todd (US)
 Location/Qualifiers
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Sig_peptide 33. -104
 BASE COUNT 243 a 516 c 480 g 211 t
 ORIGIN

Alignment Scores:
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 Score: 1894.00 Matches: 358
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US-10-001-848-3_COPY_18_375 (1-358) x AX287596 (1-1450)

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 Db 144 CGCACTGGCCGGCAGTGGCTGACTGTGCCAGTGGACGGGACCCG 203

Qy 41 ProProLeuMetProProLysAspGlyArgThrValLeuGlyArgLeuGly 60
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Qy 61 ArgValLeuProGlnGlyLeuLysValYSGlnValGluArgGluAspAlaGlyValY 80
 Db 264 CGGTGCTGCCAGGGCTGAAGGTGAAGCTGAGGGGAGATGGCGGTGTC 323

Qy 81 ValCysLysAlaThrArgGlyArgThrValLeuValLeu 100
 Db 324 GTGTGAAGGCCAACAGGCTCAGCTGAGGTCAACTACACCCCTGCTGCTG 383

Qy 101 AspAspLysSerProGlyLysGluSerLeuGlyProAspSerSerGlyGlyGlnGlu 120
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Qy 121 AspProAlaSerGlnGlnTrpAlaArgProArgPheThrGlnProSerLysMetArgArg 140
 Db 444 GACCCGGCGGCCACAGGGTCAAGGGCTCCAGATGAGTGGGGC 503
 Qy 141 ArgValIleAlaArgProValGlySerSerValArgLeuLysCysValAlaSerGlyHis 160
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 Db 624 GAGCCAGGAGAAAGTGACACTGACCTGAGAACCTGCGGAGAAGCTGAGA 681
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 Db 804 GTGGACTTCCGGGGGACCACTCCATGCAAGGTGGCAGTGACGCTGAGCTGAGCCGGTG 863
 Qy 261 IleGlnTrpLeuLysArgValGlyLutYrgIylAlaGluGlyArgHisAsnSerThrIleAsp 280
 Db 864 ATCCAGTGCTGAAAGGGTGTGAGTACGGGCTGAGGGGCCAACCTCACCATCGAT 923
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 Qy 301 SerTySerLeuAsnLysLeuLeuIleThrArgAlaArgGlnAspAlaLysMetYTrile 320
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RESULT 2
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 DEFINITION Homo sapiens, clone MGC:46034 mRNA linear PRI 26-AUG-2002
 ACCESSION BC036769
 VERSION BC036769.1 GI:22477841
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Strausberg R.
 TITLE Direct Submission
 JOURNAL Submitted (23-AUG-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC). Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
 USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 COMMENT Contact: MGChelp@mail.nih.gov
 Email: cgapbsr@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural

Db 301 QKFVYLPGDWSRDPGSVINKLITRARQDAGMYICLGANTMGSFRSAPLTVLDPK 360
 Qy 361 PPGPVASSSATSLPWPVIGIPGAVFLGTLWLCQAKKPCTPAAPAPLPGGRPP 420
 Db 361 PGPPVASSSATSLPWPVIGIPGAVFLGTLWLCQAKKPCTPAAPAPLPGGRPP 420
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 Db 421 GTARDSGDKDLPSSAALSAQPGVGLCEBHGSAPAPOHILGPFPVAGPLKLYTDIHT 480
 Qy 481 HTHTHSHTSHVEGKvQHIIHYQC 504
 Db 481 HTHTHSHTSHVEGKvQHIIHYQC 504
 XX Human; PRO; antiinflammatory; ophthalmological; vasotropics;
 DE Human PRO043.
 XX Human; PRO; antiinflammatory; ocular disease; retinitis pigmentosa;
 DE Human PRO043.
 XX Human; PRO; antiinflammatory; ophthalmological; vasotropics;
 DE Human PRO043.
 KW macular degeneration; retinal detachment; retinal tear; retinopathy;
 KW macular hole; degenerative myopia;
 KW acute retinal necrosis syndrome; traumatic chorioretinopathy;
 KW Purtscher's retinopathy; oedema; ischaemic condition;
 KW retinal vision occlusion; collagen vascular disease;
 KW thrombocytopenic purpura; uveitis; retinal vasculitis; Eales disease;
 KW systemic lupus erythematosus; environmental trauma.
 OS Homo sapiens.
 XX WO200109161 standard; Protein; 504 AA.
 PN WO200109161-A2.
 XX DT 09-APR-2002 (first entry)
 XX ID AAU81961 standard; Protein; 504 AA.
 AC AAU81961;
 XX DE Human PRO043.
 XX DT 09-APR-2002 (first entry)
 XX ID AAU81961 standard; Protein; 504 AA.
 DE Human PRO043.
 XX Human; PRO; antiinflammatory; ophthalmological; vasotropics;
 DE Human PRO043.
 KW macular degeneration; retinal detachment; retinal tear; retinopathy;
 KW macular hole; degenerative myopia;
 KW acute retinal necrosis syndrome; traumatic chorioretinopathy;
 KW Purtscher's retinopathy; oedema; ischaemic condition;
 KW retinal vision occlusion; collagen vascular disease;
 KW thrombocytopenic purpura; uveitis; retinal vasculitis; Eales disease;
 KW systemic lupus erythematosus; environmental trauma.
 OS Homo sapiens.
 XX WO200109161-A2.
 PD 08-FEB-2001.
 XX 28-JUL-2000; 2000W0-US20710.
 PF 28-JUL-2000; 2000W0-US20710.
 XX PR 28-JUL-1999; 99US-146222P.
 PR 13-SEP-1999; 99WO-US20944.
 PR 11-SEP-1999; 99WO-US21090.
 PR 29-NOV-1999; 99WO-US20214.
 PR 30-NOV-1999; 99WO-US2813.
 PR 01-DEC-1999; 99WO-US23301.
 PR 05-JAN-2000; 2000WO-US00019.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US0565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 02-MAR-2000; 2000WO-US0504.
 PR 15-MAR-2000; 2000WO-US05841.
 PR 30-MAR-2000; 2000WO-US06884.
 PR 17-MAY-2000; 2000WO-US0439.
 XX PA (GETH) GENENTECH INC.
 XX Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;
 PI Kijava JI, Latlier M, Mark MR, Marsters SA, Pitti RM;
 PI Watanabe CK, Wood WI;
 XX WPI: 2002130120/17.
 DR N-PSDB: APK28591.
 XX Promoting survival of retinal cells, or delaying or preventing retinal
 PT cell injury or death, by contacting retinal cells with PRO175, 220,
 PT 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1068 or PRO1132,
 PT polypeptide.

xx PS Claim 44; Fig 19; 152pp; English.
 xx The invention relates to promoting the survival of retinal cells, or
 cc delaying or preventing retinal cell injury or death, by contacting the
 cc peptide with the polypeptide such as the nucleic acid, a host
 cc PRO213, PRO306, PRO346, PRO322, PRO943, PRO840, PRO828, PRO826,
 cc PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids
 cc encoding the PRO proteins, a vector comprising the nucleic acid, a host
 cc cell comprising the vector, and anti-PRO antibody. The PRO proteins are
 cc useful for promoting survival of retinal cells (retinal neurons such as
 cc retinal ganglion cells, displaced retinal ganglion cells, amacrine
 cc cells, displaced amacrine cells, horizontal neurons or bipolar neurons,
 cc rod photoreceptors, or supporting cells such as Muller cells or pigment
 cc epithelial cells), or delaying or preventing retinal cell injury or
 cc death caused by ocular disease (which is or is associated with
 cc retinitis pigmentosa, macular degeneration, retinal detachment, ret-
 cc tear, retinopathy, retinal degenerative disease, macular hole,
 cc degenerative myopia, acute retinal necrosis syndrome, traumatic
 cc chorioretinopathy or contusion. Purscher's retinopathy, oedema, an-
 cc ischaemic condition, central or branch retinal vision occlusion,
 cc collagen vascular disease, thrombocytopenic purpura, uveitis, retinal
 cc vasculitis, occlusion associated with Eales disease or systemic lupus
 cc erythematosus), retinal injury or environmental trauma. The retinal
 cc cell injury or death is delayed or prevented by substantially not
 cc causing angiogenesis or mitogenesis. The present sequence represents
 cc a PRO protein.

xx Sequence 504 AA;

xx SQ Query Match 100.0%; Score 2709; DB 23; Length 504;
 xx Best Local Similarity 100.0%; Pred. No. 7.3e-16;
 xx Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTPSPILLPLPLPILLGFPAAARGPKMDKVPVPROVARLGRTRVQCPVEGDPPL 60
 Db 1 MTPSPILLPLPLPILLGFPAAARGPKMDKVPVPROVARLGRTRVQCPVEGDPPL 60
 Qy 61 TMATTKDGRTHGMSRERVFLPQGKVKQVEREDAGVYCKATNGFGLSVNNTYLAVLVDI 120
 Db 61 TMATTKDGRTHGMSRERVFLPQGKVKQVEREDAGVYCKATNGFGLSVNNTYLAVLVDI 120
 Qy 121 SPGKESLGPDSSSGQEDPASQWARPRTPQSPMRRVTPARPGSSVPLKCYASGHPRP 180
 Db 121 SPGKESLGPDSSSGQEDPASQWARPRTPQSPMRRVTPARPGSSVPLKCYASGHPRP 180
 Qy 121 DITMKDDQQLTRPAAABPKKWTLSLKLRLPDSGKTCRVSNRAGINATYKVDVJQ 240
 Db 121 DITMKDDQQLTRPAAABPKKWTLSLKLRLPDSGKTCRVSNRAGINATYKVDVJQ 240
 Qy 241 RTRSKVPLGTHPATTVDGGITTSFOCKVRSRDPVTLKREVEYAGBGRNSTIDVG 300
 Db 241 RTRSKVPLGTHPATTVDGGITTSFOCKVRSRDPVTLKREVEYAGBGRNSTIDVG 300
 Qy 301 QKFVVLPTGWDWSRDGSVINKLITRAODDAGMYICGANTMGYSFSASAFLTVLPDK 360
 Db 301 QKFVVLPTGWDWSRDGSVINKLITRAODDAGMYICGANTMGYSFSASAFLTVLPDK 360
 Qy 361 PPGPPVASSSSATSLPWPVYIGIPGAVFLGTLWLCQAKKPCTPAPAPLPGHRPP 420
 Db 361 PPGPPVASSSSATSLPWPVYIGIPGAVFLGTLWLCQAKKPCTPAPAPLPGHRPP 420
 Qy 421 GTARDSGDKDLPSSAALSGPGVGLCBHGSAPAQHILGPGBVAGPKLYPDHT 480
 Db 421 GTARDSGDKDLPSSAALSGPGVGLCBHGSAPAQHILGPGBVAGPKLYPDHT 480
 Qy 481 HTHTHSHTSHVEGKvQHIIHYQC 504
 Db 481 HTHTHSHTSHVEGKvQHIIHYQC 504

RESULT 8
 ABU59072

